

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:20:13 ; Search time 52.2 Seconds
(without alignments)
27.316 Million cell updates/sec

Title: US-09-331-631a-38

Sequence: 1 CXXXCXXXXXXXXXXXXXXC 21

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	30	2 A38933	vitronectin - bovi
2	53	100.0	37	2 E44007	aptoctoxin III - tr
3	53	100.0	39	1 IZMS	cygnin - black swa
4	53	100.0	40	2 JX0070	melagrin - turkey
5	53	100.0	55	2 S25774	testis-specific pr
6	53	100.0	57	1 SMK025	metallochionein 2
7	53	100.0	57	2 S59073	metallochionein 1s
8	53	100.0	58	1 SMK015	metallochionein 1
9	53	100.0	58	2 S59072	metallochionein 1s
10	53	100.0	58	2 A37039	metallochionein 1
11	53	100.0	58	2 S43367	metallochionein -
12	53	100.0	63	2 S25772	testis-specific pr
13	53	100.0	63	2 A34484	metallochionein 1
14	53	100.0	66	2 T18117	hypothetical prote
15	53	100.0	68	2 S25775	testis-specific pr
16	53	100.0	70	1 XISR1A	insect toxin 1 - s
17	53	100.0	70	1 S08267	toxin 1 - scorpion
18	53	100.0	72	2 S39416	metallochionein 10
19	53	100.0	72	2 S39418	metallochionein 10
20	53	100.0	72	2 S39419	metallochionein 10
21	53	100.0	72	2 S39417	metallochionein 10
22	53	100.0	74	2 S25773	testis-specific pr
23	53	100.0	83	2 A49763	midgut expression
24	53	100.0	84	2 J01356	VI protein - Misca
25	53	100.0	88	2 G34444	insect toxin 2 pre
26	53	100.0	95	1 KRDKF4	keratin B-4, feath
27	53	100.0	95	1 KRPFY4	keratin B-4, feath
28	53	100.0	98	1 KRCHP1	keratin I, feather
29	53	100.0	98	1 KRCHP2	keratin II, feathe

30	53	100.0	98	1 KRGLBS	keratin, feather -
31	53	100.0	98	2 S06807	keratin, feather (
32	53	100.0	98	2 S06806	keratin, feather (
33	53	100.0	98	2 S06808	keratin, feather (
34	53	100.0	105	2 S64495	hypothetical prote
35	53	100.0	107	2 T17698	tap1 protein - gar
36	53	100.0	107	2 T27988	hypothetical prote
37	53	100.0	117	2 S24023	dopamine receptor
38	53	100.0	117	2 S24194	dopamine receptor
39	53	100.0	117	2 S24195	dopamine receptor
40	53	100.0	118	2 S26689	hypothetical prote
41	53	100.0	135	2 T15610	hypothetical prote
42	53	100.0	137	2 T15609	hypothetical prote
43	53	100.0	151	2 S60314	hair keratin cyste
44	53	100.0	152	2 T18975	hypothetical prote
45	53	100.0	153	2 PN0564	von Willebrand fac

ALIGNMENTS

RESULT 1
A38933
vitronectin - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 05-Apr-1995 #sequence_revision 05-Apr-1995 #text_change 07-May-1999
R:Hayman, E.G.; Pierschbacher, M.D.; Suzuki, S.; Ruoslahti, E.
Exp. Cell Res. 160, 245-258, 1985
A:Title: Vitronectin-a major cell attachment-promoting protein in fetal bovine serum
A:Reference number: A38933; WUID:86005161
A:Accession: A38933
A:Molecule type: protein
A:Residues: 1-30 <HAY>
R:Mimuro, J.; Loskutoff, D.J.
J. Biol. Chem. 264, 936-939, 1989
A:Title: Purification of a protein from bovine plasma that binds to type 1 plasminoge
ctin.
A:Reference number: A32200; WUID:89093166
A:Accession: A32200
A:Molecule type: protein
A:Residues: 1-4, 'X', 6-8, 'X', 10-18, 'X', 20, 'X', 22-24, 'X', 26-28 <MIM>
R:Nakashima, N.; Miyazaki, K.; Ishikawa, M.; Yatonjo, T.; Ogawa, H.; Uchiyori, H.; Ma
Blochin. Biophys. Acta 1120, 1-10, 1992
A:Title: Vitronectin diversity in evolution but uniformity in ligand binding and size
A:Reference number: S21768; WUID:92207982
A:Accession: S22231
A>Status: preliminary
A:Molecule type: protein
A:Residues: 'X', 2-4, 'X', 6-8, 'X', 10-18, 'X', 20, 'X' <NAK>
R:Seifert, D.; Loskutoff, D.J.
Biochim. Biophys. Acta 1078, 23-30, 1991
A:Title: Kinetic analysis of the interaction between type 1 plasminogen activator inh
of bovine vitronectin.
A:Reference number: S15978; WUID:91265534
A:Accession: S15978
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-4, 'X' <SEI>
C:Superfamily: vitronectin; hemopexin repeat homology; somatomedin B homology
C:Keywords: cell adhesion; heparin binding

Query Match 100.0%; Score 53; DB 2; Length 30;

Best local similarity 23.8%; Pred. No. 1.3e+02;

Matches 5; Conservative 16; Mismatches 0; Indels 0; Caps 0;

OY 1 CXXXCXXXXXXXXXXXXXXC 21

DB 5 CKGRCTGFYATRCQCDELIC 25

RESULT 2

E44007
aptoctoxin III - trap-door spider (Aptostichus sp.)
N:Alternate names: insecticidal peptide Aps III
C:Species: Aptostichus sp.
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C:Accession: E44007
R:Skinner, W.S.; Dennis, P.A.; Li, J.P.; Quistad, G.B.
Toxicolom 30, 1043-1050, 1992
A:Title: Identification of insecticidal peptides from venom of the trap-door spider, Aptostichus
A:Reference number: A44007; MUID:93069259
A:Accession: E44007
A:Molecule type: protein
A:Residues: 1-37 <SKI>
A:Cross-references: PIDN:AAB24051.I; PID:9259281
A:Note: the source is designated as Aptostichus schlinger!
A:Note: sequence extracted from NCBI backbone (MCBIF:119526)
C:Keywords: disulfide bond;; toxin; venom

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Query Match          100.0%  Score 53:  DB 2:  Length 37:
Best Local Similarity 19.0%  Pred. No. 1.4e+02:
Matches 4:  Conservative 17:  Mismatches 0:  Indels 0:
                                Gaps 0:

Oy  1  CXXXXXXXXXXXXXXXXCXXC 21
    |::|::|::|::|::|::|::|
Db   15  CGGCAATWMCITGGGCCSTC 35

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RESULT      3
I2MS
cygnin - black swan
C:Species: Cygnus altratus (black swan)
C:Date: 18-Apr-1984 #sequence_revision 28-Feb-1986 #text_change 24-Nov-1999
C:Accession: A03258
R:Simpson, R.J.: Morgan, F.J.
Submitted to the Atlas, November 1982
A:Reference number: A94600
A:Accession: A03258
A:Molecule type: protein
A:Residues: 1-39 <SIM>
C:Comment: Cygnin shows some similarity to the amino-terminal fragment of the carboxyl-terminus of the protein
C:Superfamily: cygnin
C:Keywords: blocked amino end; egg white
P:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status 1

```

Query Match	100.0%	Score 53;	DB 1;	Length 39;
Best Local Similarity	19.0%;	pred No. 1.4e+02;		
Best Matches	4;	Conservative 17;	Mismatches 0;	Indels 0;
			Gaps	0;

QY	1	CXXXCXXXXXXXXXXCXXC	21
		:: ::: ::: :::	
Db	12	CSSKCSKADVWSLSSDCKFYC	32

RESULT
JX0070

```

meleagrln - turkey
N:Alternate names: cygnin homolog
C:Species: Meleagris gallopavo (common turkey)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 05-Aug-1994
C:Accession: JX0070
R:Odani, S.; Koide, T.; Ono, T.; Takahashi, Y.; Suzuki, J.
J. Biochem. 105, 660-663, 1989
A:Title: Covalent structure of a low-molecular-mass protein, meleagrln, present in a turkey
A:Reference number: JX0070; MUID:89340398
A:Accession: JX0070
A:Molecule type: protein
A:Residues: 1-40 <ODA>
A:Superfamily: cygnin
C:Keywords: egg white; pyroglutamic acid
E:I/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:6-32,16-33/Disulfide bonds: (or 6-33, 16-32) #status predicted

```

F;12-28/Disulfide bonds: #status experimental

Query Match	100.0%;	Score 53;	DB 2;	length 40;
Best Local Similarity	19.0%;	Pred. No. 1.5e+02;		
Matches	4;	Conservative	17;	Mismatches 0;
			Indels	0;
			Gaps	0;

```
QY 1 CXXXXXXXXXXXXXXCXXX 21
    |::|:::|:::|:::|
Db 12 CSSKCSKAEWAYSPDCKVHC 32
```

RESULT 5
005774

5257114
 testis-specific protein Mst84Dc - fruit fly (*Drosophila melanogaster*)
 C:Species: *Drosophila melanogaster*
 C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 20-Aug-1999
 C:Accession: S257774; C56565
 R:Kuhn, R.; Kuhn, C.; Boersch, D.; Glaetzer, K.H.; Schaefer, U.; Schaefer, M.
 Mech. Dev. 35, 143-151, 1991
 A:Title: A cluster of four genes selectively expressed in the male germ line of *Drosophila*
 A:Reference number: A56565; MUID:92102953
 A:Accession: S25774
 A:Molecule type: DNA
 A:Residues: 1-55 <Kun>
 A:Cross-references: EMBL:X67703; NID:g11072; PIDN:CAA47939.1; PID:g11075
 A:Note: The authors translated the codon TGC for residue 55 as Thr
 A:Note: sequence extracted from NCBI backbone (NCBIIN:74217, NCBIIP:74222)
 A:Genetics:
 A:Gene: Mst84Dc
 A:Cross-references: FlyBase:FBgn0004174
 A:Map position: 3
 C:Superfamily: fruit fly testis-specific protein
 :Keywords: spermatogenesis; tandem repeat

Query Match	100.0%;	Score 53;	DB 2;	Length 55;
Best Local Similarity	19.0%;	Pred. No. 1.7e+02;		
Matches	4;	Conservative 17;	Mismatches 0;	Indels 0;
				Gaps 0;

```
QY 1 CXXXXXXXXXXXXXXCXXC 21
    |::|:::|:::|:::|
Db 2 CCGPCGSCCGYCCGPGCGPC 22
```

RESULT 6

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smkuzs
metallothionein 2 - mud crab
C:Species: Scylla serrata (mud crab)
C:Date: 19-Feb-1984 #sequence_revision 19-Feb-1994 #text_change 13-Sep-1996
C:Accession: A03284
R:Leitch, K.; Ammer, D.; Olafson, R.W.
J. Biol. Chem. 257, 2420-2426, 1982
A:Title: Crab metallothionein. Primary structures of metallothioneins 1 and 2.
A:Reference number: A92363; M0ID:82142340
A:Accession: A03284
A:Molecule type: protein
A:Residues: 1-57 <LRR>
C:Superfamily: metallothionein
C:Keywords: metal binding

```

Query Match	100.0%;	Score 53;	DB 1;	length 57;
Best Local Similarity	19.0%;	Pred. NO. 1.8e+02;		
Matches	4;	Conservative 17;	Mismatches 0;	Indels 0;
			Gaps 0;	

```
Qy 1 CXXXXXXXXXXXXXXXXCXXXC 21
    |::|:::|:::|:::|:::|
Db 33 CSSGCKCANKEDCRKTCSPC 53
```

RESULT
S59073

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metallothionein isoform IIA - blue crab
C:Species: Callinectes sapidus (blue crab)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
C:Accession: S59073
R:Browner, M.; Enghild, J.; Hoexum-Brouwer, T.; Thogersen, I.; Truncali, A.
Biochem. J. 311, 617-622, 1995
A:Title: Primary structure and tissue-specific expression of blue crab (Callinectes sapidus) metallothionein
A:Reference number: S59072; MUID:96033062
A:Accession: S59073
A:Molecule type: protein
A:Residues: 1-57 <BRO>
C:Superfamily: metallothionein
C:Keywords: metal binding

Query Match          100.0%; Score 53; DB 2; Length 57;
Best Local Similarity 19.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXCXXXXXXXXXXCXXXC 21
   |::|::|::|::|::|::|::|
DB 33 CSSECKCTSKKECKSKTKCK 53

RESULT 8
SMKD1S
metallothionein 1 - mud crab
C:Species: Scylla serrata (mud crab)
C:Date: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 13-Sep-1996
C:Accession: A03283
R:lerch, K.; Ammer, D.; Olafson, R.W.
J. Biol. Chem. 257, 2420-2426, 1982
A:Title: Crab metallothionein. Primary structures of metallothioneins 1 and 2.
A:Reference number: A92363; MUID:82142340
A:Accession: A03283
A:Molecule type: protein
A:Residues: 1-58 <LEKR>
A:Note: The five Cys-X-Cys sequences are believed to be the principal metal-binding sites
C:Superfamily: metallothionein
C:Keywords: metal binding

Query Match          100.0%; Score 53; DB 1; Length 58;
Best Local Similarity 19.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXCXXXXXXXXXXCXXXC 21
   |::|::|::|::|::|::|::|
DB 33 CSSGCKCANKECKSKTKCK 53

RESULT 9
S59072
metallothionein isoform Ia - blue crab
C:Species: Callinectes sapidus (blue crab)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
C:Accession: S59072
R:Browner, M.; Enghild, J.; Hoexum-Brouwer, T.; Thogersen, I.; Truncali, A.
Biochem. J. 311, 617-622, 1995
A:Title: Primary structure and tissue-specific expression of blue crab (Callinectes sapidus) metallothionein
A:Reference number: S59072; MUID:96033062
A:Accession: S59072
A:Molecule type: protein
A:Residues: 1-58 <BRO>
C:Superfamily: metallothionein
C:Keywords: metal binding

Query Match          100.0%; Score 53; DB 2; Length 58;
Best Local Similarity 19.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXCXXXXXXXXXXCXXXC 21

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```

|:::|
Db      33  CTSCKCATKECKSTCTKPC  53

RESULT  10
A37039
metallothionein 1 - American lobster
C:Species: Homarus americanus (American lobster)
C:Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 12-Apr-1995
C:Accession: A37039
R:Brower, M.; Winge, D.R.; Gray, W.R.
J. Inorg. Biochem. 35, 289-303, 1989
A:Title: Structural and functional diversity of copper-metallothioneins from the Amer
A:Reference number: A37039; MUID:89215793
A:Accession: A37039
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-58 <BRO>
C:Superfamily: metallothionein

Query Match      100.0%; Score 53; DB 2; Length 58;
Best Local Similarity 19.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

QY      1  CXXCXXXXXXXXXXCXXC  21
|:::|
Db      33  CTSCKCPSKDECAKTCCKPC  53

RESULT  11
S43367
metallothionein - green crab
C:Species: Carcinus maenas (green crab, common shore crab)
C:Date: 19-Mar-1997 #sequence_revision 01-Feb-1999 #text_change 07-May-1999
C:Accession: S43367
R:Pedersen, K.L.; Pedersen, S.N.; Hojrup, P.; Andersen, J.S.; Koepstorff, P.; Knudsen
Biochem. J. 297, 609-614, 1994
A:Title: Purification and characterization of a cadmium-induced metallothionein from
A:Reference number: S43367; MUID:94153337
A:Accession: S43367
A:Molecule type: protein
A:Residues: 1-58 <PED>
A:Note: The sequence from Fig. 4 is inconsistent with that from Fig. 6 in having an a
C:Superfamily: metallothionein
C:Keywords: metal binding; chelation; metal-thiolate cluster
F:6,12,17,21,28/Binding site: transition metal ions (Cys) #status predicted
F:31,38,46,47,54,56,57/Binding site: transition metal ions (Cys) #status predicted

Query Match      100.0%; Score 53; DB 2; Length 58;
Best Local Similarity 19.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

QY      1  CXXCXXXXXXXXXXCXXC  21
|:::|
Db      34  CSSGCKCTTKEDCKCTCKPC  54

RESULT  12
S25772
testis-specific protein Mst84da - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 20-Aug-1999
C:Accession: S25772; A56565
R:Kuhn, R.; Kuhn, C.; Boersch, D.; Glaetter, K.H.; Schaefer, U.; Schaefer, M.
Mech. Dev. 35, 143-151, 1991
A:Title: A cluster of four genes selectively expressed in the male germ line of Dros
A:Reference number: A56565; MUID:92102953
A:Accession: S25772
A:Molecule type: DNA
A:Residues: 1-63 <KUH>
A:Cross-references: EMBL:X67703; NID:g11072; PIDN:CAA47937.1; PID:g11073

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